


includes CCP (Saccharomyces cerevisiae-derived cytochrome C peroxidase) (SEQ ID NO. 10) and ECP (E. coli-derived peroxidase) (SEQ ID NO. 11) as Class I peroxidases. Comparison was done with ARP (Arthromyces ramosus-derived peroxidase) (SEQ ID NO. 12), MnP (manganic peroxidase derived from a fungus of the genus Phanerochaete) (SEQ ID NO. 13) and LiP (Phanerochaete chrysosporium-derived lignin peroxidase) (SEQ ID NO. 14) as Class II peroxidases. Additionally, Class III peroxidase includes TP (Tunip peroxidase) (SEQ ID NO. 15) and HRP (horse radish peroxidase) (SEQ ID NO. 16). The sequences of the sequence comparison shown in Figure 4 are not the full amino acid sequences of each polypeptide, but rather parts thereof. Further, some sequences of the sequence comparison in Figure 4 include non-consecutive amino acids of their corresponding full-length polypeptide. In Figure 4, the number located above the amino acid in each sequence depicts the position of that amino acid as it resides within the full-length polypeptide.--

Page 36 (Abstract), after the last line, beginning on the next page, replace the

 Sequence Listing at pages 1-8 with the substitute Sequence Listing attached hereto.

REMARKS

Claims 1-6 are active in the present application.

Applicants have now submitted a substitute Sequence Listing and a corresponding computer-readable Sequence Listing. Contents of the paper copy of the substitute Sequence Listing and the computer-readable Sequence Listing are identical. Support for all the sequences listed in the substitute Sequence Listing can be found in the present application. No new matter is introduced by the submission of the substitute Sequence Listing and the computer-readable Sequence Listing.

The specification is amended to clarify the nature of the sequences of the sequence comparison depicted in Figure 4 and in the substitute Sequence Listing. No new matter is believed to be introduced by the amendment.

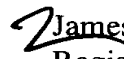
Applicants submit that this application is in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.

A handwritten signature in black ink, appearing to read 'Norman F. Oblon', with the number '36379' written to its right.

Norman F. Oblon
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Marked-Up Copy
Serial No: 09/926,084
Amendment Filed on:
HEREWITH

IN THE SPECIFICATION

Please amend the specification as follows:

Please replace the paragraph at page 32, line 18, to page 33, line 8, as follows:

--The classification by Welinder et al. is based on the comparison of highly common sequences in the primary sequence of each peroxidase. In more detail, the classification is practiced by comparing the primary sequences around the His residue proximal to the heme iron and the His and Arg residues distal to the heme iron. Using the sequence comparison table prepared by Welinder et al., the DyP sequence was compared (Fig. 4). Herein, Fig. 4 includes CCP (Saccharomyces cerevisiae-derived cytochrome C peroxidase) (SEQ ID NO. 10) and ECP (E. coli-derived peroxidase) (SEQ ID NO. 11) as Class I peroxidases. Comparison was done with ARP (Arthromyces ramosus-derived peroxidase) (SEQ ID NO. 12), MnP (manganic peroxidase derived from a fungus of the genus Phanerochaete) (SEQ ID NO. 13) and LiP (Phanerochaete chrysosporium-derived lignin peroxidase) (SEQ ID NO. 14) as Class II peroxidases. Additionally, Class III peroxidase includes TP (Tunip peroxidase) (SEQ ID NO. 15) and HRP (horse radish peroxidase) (SEQ ID NO. 16). The sequences of the sequence comparison shown in Figure 4 are not the full amino acid sequences of each polypeptide, but rather parts thereof. Further, some sequences of the sequence comparison in

Figure 4 include non-consecutive amino acids of their corresponding full-length polypeptide.

In Figure 4, the number located above the amino acid in each sequence depicts the position of that amino acid as it resides within the full-length polypeptide.--